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	130	140	150	160	
1093	GGGGAAACCCAGCACGAGTGTCTGTC	CTACCCGCAT	CT	M.tuberculosis	
422	GGGGAAACCCAGCACGAGTGTCTGTC	CTACCCG	TATCT	M.avium	
422	GGGGAAACCCAGCACGAGTGTCTGTC	CTACCCG	TATCT	M.paratuberc.	
507	GGGGAAACCCAGCACGAGTGTCTGTC	CTACCCG	ACCT	M.phlei	
432	GGGGAAACCCAGCACGAGTGTCTGTC	CTACCCG	TATCT	M.leprae	
207	GGGGAAACCCAGCACGAGTGTCTGTC	CTACCCG	TATCT	M.gastri	
150	GGGGAAACCCAGCACGAGTGTCTGTC	CTACCCG	CATCT	M.kansasii	
2588	GGGGAAACCCAGCACGAGTGTCTGTC	CTACCCG	GCCT	M.smegmatis	

	210	220	230	240	
1172	CATCTCAGTACCCGTAGGA	GGAGAAAACAATTGTGATTCC		M.tuberculosis	
501	CATCTCAGTACCCGTAGGA	GGAGAAAACAATTGTGATTCC		M.avium	
501	CATCTCAGTACCCGTAGGA	GGAGAAAACAATTGTGATTCC		M.paratuberc.	
586	CATCTCAGTACCCGTAGGA	AGAGAGAAAACAATTGTGATTCC		M.phlei	
511	CATCTCAGTACCCGTAGGA	AGAGAGAAAACAATTGTGATTCC		M.leprae	
286	CATCTCAGTACCCGTAGGA	AGAGAGAAAACAATTGTGATTCC		M.gastri	
229	CATCTCAGTACCCGTAGGA	AGAGAGAAAACAATTGTGATTCC		M.kansasii	
2667	CATCTCAGT	CCCCGTAGGA	AGAGAGAAAACAATTGTGATTCC	M.smegmatis	

	330	340	350	360	
1289	TGTGGGA	G-GATATGTCTCAGCGCTACCCGGCTGAGA- <u>GG</u>		M.tuberculosis	
617	TGTGGGATT	GATATGTCTCAGC	CTACCTGGCTGAGG- <u>GG</u>	M.avium	
617	TGTGGGATT	GATATGTCTCAGC	CTACCTGGCTGAGG- <u>GG</u>	M.paratuberc.	
703	TGTGGGGCTGTC	TCAGCGCTCCGCCGGC	GATGGCAG	M.phlei	
629	TGTGGGATT	GATATGTCTCAGC	CTACCTGGCTGAGG- <u>GG</u>	M.leprae	
404	TGTGGGATCGATA	CGTCTCAGC	CTACCCGGCTGAGG- <u>GG</u>	M.gastri	
347	TGTGGGATCGATA	CGTCTCAGC	CTACCCGGCTGAGG- <u>GG</u>	M.kansasii	
2785	TGTGGGACCT	ATCTCGG	CTACCTGGCTG	GAGGG M.smegmatis	

Figure 1A

	370	380	390	400	
1327	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGAT				M.tuberculosis
656	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGAT				M.avium
656	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGAT				M.paratuberc.
742	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGAT				M.phlei
668	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGAT				M.leprae
443	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGAT				M.gastri
386	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGAT				M.kansasii
2823	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGAT				M.smegmatis
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	450	460	470	480	
1406	CGGCACCTGCCCTAGTATCAATTCCCGAGTAGCAGCGGGCC				M.tuberculosis
735	CGGCACCTGCCCTATATCAACACCCGAGTAGCAGCGGGCC				M.avium
735	CGGCACCTGCCCTATATCAACACCCGAGTAGCAGCGGGCC				M.paratuberc.
820	TGCTGCCCTGTCACAGG-TCCCGAGTAGCAGCGGGCC				M.phlei
747	TGGCACCTGCCCTGATCAATTCCCGAGTAGCAGCGGGCC				M.leprae
522	CGGCACCTGCCCTGATCAATTCCCGAGTAGCAGCGGGCC				M.gastri
465	CGGCACCTGCCCTGATCAATTCCCGAGTAGCAGCGGGCC				M.kansasii
2902	CGACCTCTGCTGATGGTTCCCGAGTAGCAGCGGGCC				M.smegmatis
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	490	500	510	520	
1446	CGTGGAAATCGCTGTGAATCGCCGGGACCACCGGTAAG				M.tuberculosis
775	CGTGGAAATCGCTGTGAATCGCCGGGACCACCGGTAAG				M.avium
775	CGTGGAAATCGCTGTGAATCGCCGGGACCACCGGTAAG				M.paratuberc.
857	CGTGGAAATCGCTGTGAATCGCCGGGACCACCGGTAAG				M.phlei
787	CGTGGAAATCGCTGTGAATCGCCGGGACCACCGGTAAG				M.leprae
562	CGTGGAAATCGCTGTGAATCGCCGGGACCACCGGTAAG				M.gastri
505	CGTGGAAATCGCTGTGAATCGCCGGGACCACCGGTAAG				M.kansasii
2942	CGTGGAAATCGCTGTGAATCGCCGGGACCACCGGTAAG				M.smegmatis

Figure 1B

3/31

	610	620	630	640	
1566	GTACCTGAAACCGTGTGCCTACAATCCGTCAAGAGC	TCCT	M. tuberculosis		
894	GTACCTGAAACCGTGTGCCTACAATCCGTCAAGAGC	TCCT	M. avium		
894	GTACCTGAAACCGTGTGCCTACAATCCGTCAAGAGC	TCCT	M. paratuberc.		
976	GTACCTGAAACCGTGTGCCTACAATCCGTCAAGAGC	TCCT	M. phlei		
907	GTACCTGAAACCGTGTGCCTACAATCCGTCAAGAGC	TCCT	M. leprae		
682	GTACCTGAAACCGTGTGCCTACAATCCGTCAAGAGC	TCCT	M. gastri		
625	GTACCTGAAACCGTGTGCCTACAATCCGTCAAGAGC	TCCT	M. kansasii		
3062	GTACCTGAAACCGTGTGCCTACAATCCGTCAAGAGC	TCCT	M. smegmatis		
	650	660	670	680	
1606	TTTCCTCTCCGGAGGGTGATGGCGTGCCTTTGA		M. tuberculosis		
934	C-----GIGGGGTGATGGCGTGCCTTTGA		M. avium		
934	C-----GIGGGGTGATGGCGTGCCTTTGA		M. paratuberc.		
1016	CTT-----GAGTGGGGTGATGGCGTGCCTTTGA		M. phlei		
947	T-----GIGGGGTGATGGCGTGCCTTTGA		M. leprae		
722	T-----GIGGGGTGATGGCGTGCCTTTGA		M. gastri		
665	C-----GIGGGGTGATGGCGTGCCTTTGA		M. kansasii		
3102	ACGTGT-----GIGGGGTGATGGCGTGCCTTTGA		M. smegmatis		
	690	700	710	720	
1646	AGAATGAGCCTGCAGTCAGGGACATGTCGCAAGGTTAAC		M. tuberculosis		
4	AGAATGAGCCTGCAGTCAGGGACATGTCGCAAGGTTAAC		M. bovis		
959	AGAATGAGCCTGCAGTCAGGGACATGTCGCAAGGTTAAC		M. avium		
23	AGAATGAGCCTGCAGTCAGGGACATGTCGCAAGGTTAAC		M. intracellulare		
959	AGAATGAGCCTGCAGTCAGGGACATGTCGCAAGGTTAAC		M. paratuberc.		
1046	AGAATGAGCCTGCAGTCAGGGACATGTCGCAAGGTTAAC		M. phlei		
972	AGAATGAGCCTGCAGTCAGGGACATGTCGCAAGGTTAAC		M. leprae		
747	AGAATGAGCCTGCAGTCAGGGACATGTCGCAAGGTTAAC		M. gastri		
690	AGAATGAGCCTGCAGTCAGGGACATGTCGCAAGGTTAAC		M. kansasii		
3132	AGAATGAGCCTGCAGTCAGGGACATGTCGCAAGGTTAAC		M. smegmatis		

Figure 1C

4/31

	770	780	790	800	
1726	GACCCACACGGCGATA	CGCGCTGTGA	AATAGTGGCGTGT		M. tuberculosis
84	CGACCCACACGGCGATA	CGCGCTGTGA	AATAGTGGCGTGT		M. bovis
1039	CGCAT	CGCTTTGGGGTGT		AGTGGCGTGT	M. avium
103	CGCAT	CGCTTTGGGGTGT		AGTGGCGTGT	M. intracellulare
1039	CGCAT	CGCTTTGGGGTGT		AGTGGCGTGT	M. paratuberculosis
1126	CGTAT	CAACCTGTTGGGGTGT		AGTGGCGTGT	M. phlei
1052	CGTAT	CACG	TGAGCGTG	GTGT	AGTGGCGTGT M. leprae
827	CGTAT	CACGCGT	TAAGCGTG	GTGT	AGTGGCGTGT M. gastri
770	CGTAT	CGCGCGAGCGTG	GTGT		AGTGGCGTGT M. kansasii
3212	CGTAT	CCACACAAAGAGTGTGTG	GTGT		AGTGGCGTGT M. smegmatis

	970	980	990	1000	
1926	ATTTAGGTGCAGCGTTGCGTGGTTCACCG	CGGGAGGTAGAG			M. tuberculosis
1228	ATTTAGGTGCAGCGTTGCGTGGTTCACCG	CGGGAGGTAGAG			M. avium
1228	ATTTAGGTGCAGCGTTGCGTGGTTCACCG	CGGGAGGTAGAG			M. paratuberculosis
1322	ATTTAGGTGCAGCGT	CGCGT	TTATCGGAGGTAGAG		M. phlei
1244	ATTTAGGTGCAGCGTTGCGTGGTTCACCG	CGGGAGGTAGAG			M. leprae
1019	ATTTAGGTGCAGCGTTGCGTGT	TTTCACCG	CGGGAGGTAGAG		M. gastri
962	ATTTAGGTGCAGCGTTGCGTGT	TTTCACCG	CGGGAGGTAGAG		M. kansasii
3408	ATTTAGGTGCAGCGT	CGCGT	TTGCGGGAGGTAGAG		M. smegmatis

	1050	1060	1070	1080	
2005	CAGCCAAACTCCGAATGCCG-TGGTG	TA	AAGCGTGGCA		M. tuberculosis
1307	CAGCCAAACTCCGAATGCCG-TGGTG	TA	AAGCGTGGCA		M. avium
1307	CAGCCAAACTCCGAATGCCG-TGGTG	TA	AAGCGTGGCA		M. paratuberculosis
1401	CAGCCAAACTCCGAATGCCG	TAAG	TGAAAG	GTGGCA	M. phlei
1323	CAGCCAAACTCCGAATGCCG-TGGTG	TA	AAGCGTGGCA		M. leprae
1098	CAGCCAAACTCCGAATGCCG-TGGTG	TA	AAGCGTGGCA		M. gastri
1041	CAGCCAAACTCCGAATGCCG-TGGTG	TA	AAGCGTGGCA		M. kansasii
3486	CAGCCAAACTCCGAATGCCG	TAAGG	CGAAGAG	TGGGA	M. smegmatis

Figure 1D

	1130	1140	1150	1160	
2082	ACAGCCCAGATCGCCGGCTAAGGCCCC	AAGCGTGTGCTA	M.tuberculosis		
1385	ACAGCCCAGATCGCCGGCTAAGGCCCC	AAGCGTGTGCTA	M.avium		
1385	ACAGCCCAGATCGCCGGCTAAGGCCCC	AAGCGTGTGCTA	M.paratuberc.		
1479	ACAGCCCAGATCGCCGGCTAAGGCCCC	AAGCGTGTGCTA	M.phlei		
1401	ACAGCCCAGATCGCCGGCTAAGGCCCC	AAGCGTGTGCTA	M.leprae		
1175	ACAGCCCAGATCGCCGGCTAAGGCCCC	AAGCGTGTGCTA	M.gastri		
1118	ACAGCCCAGATCGCCGGCTAAGGCCCC	AAGCGTGTGCTA	M.kansasii		
3566	ACAGCCCAGATCGCCGGCTAAGGCCCC	AAGCGTGTGCTA	M.smegmatis		
<hr/>					
	1290	1300	1310	1320	
2241	CTCAAGCACACCGCCGAAGCCGGCACAT	CCACCTTGT-	M.tuberculosis		
1544	CTCAAGCACACCGCCGAAGCCGGCACAT	TCATCTT-TA	M.avium		
1544	CTCAAGCACACCGCCGAAGCCGGCACAT	TCATCTT-TA	M.paratuberc.		
1638	CTCAAGCACACCGCCGAAGCCGGCACAT	-ATCAGCCTT-TG	M.phlei		
1560	CTCAAGCACACCGCCGAAGCCGGCACAT	-TCACCTT-TA	M.leprae		
1334	CTCAAGCACACCGCCGAAGCCGGCACAT	--ACC-GC--A	M.gastri		
1277	CTCAAGCACACCGCCGAAGCCGGCACAT	--ACC-GC--A	M.kansasii		
3726	CTCAAGCACACCGCCGAAGCCGGCACAT	-GCCACCTT-TG	M.smegmatis		
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	1330	1340	1350	1360	
2280	-GGTGGGTG	TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.tuberculosis		
1583	CGGTGGATGTGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.avium			
1583	CGGTGGATGTGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.paratuberc.			
1676	TGGCTGGTGTGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.phlei			
1600	GGGTGGATGTGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.leprae			
1367	AGGT-----TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.gastri			
1310	AGGT-----TGGGTAGGGGAGCGTCCCTCATTCAGCGAAG	M.kansasii			
3764	TT-----TGGGTAGGGGAGCGTCCATTCAGCGAAG	M.smegmatis			

Figure 1E

6/31

	1370	1380	1390	1400	
2319	CCACGGGTGACCGGTGGTGGAGGGTGAGTGAGAAT				M.tuberculosis
1623	CTCCGGGTGACCGGTGGTGGAGGGTGAGTGAGAAT				M.avium
1623	CTCCGGTGATCGGTGGTGGAGGGTGAGTGAGAAT				M.paratuberc.
1716	CCGCCGAGTGAATCGGTGGTGGAGGGTGAGTGAGAAT				M.phlei
1640	CCTCCGGGTGACCGGTGGTGGAGGTGGAGTGAGAAT				M.leprae
1402	CCGCCGGGTGACCGGTGGTGGAGGTGGAGTGAGAAT				M.gastri
1345	CTGCCGGGTGACCGGTGGTGGAGGTGGAGTGAGAAT				M.kansasii
3796	CCGCCGAGTATCGAGTGGTGGAGGGTGAGTGAGAAT				M.smegmatis
	1410	1420	1430	1440	
2359	GCAGGCATGAGTAGCGATAAGGCAAGTGAGAACCTTCCC				M.tuberculosis
1662	GCAGGCATGAGTAGCGATAAGGCAAGTGAGAACCTTCCC				M.avium
1662	GCAGGCATGAGTAGCGATAAGGCAAGTGAGAACCTTCCC				M.paratuberc.
1756	GCAGGCATGAGTAGCGATAAGGCAAGTGAGAACCTTCCC				M.phlei
1680	GCAGGCATGAGTAGCGATAAGGCAAGTGAGAACCTTCCC				M.leprae
1442	GCAGGCATGAGTAGCGATAAGGCAAGTGAGAACCTTCCC				M.gastri
1385	GCAGGCATGAGTAGCGATAAGGCAAGTGAGAACCTTCCC				M.kansasii
3836	GCAGGCATGAGTAGCGATAAGGCAAGTGAGAACCTTCCC				M.smegmatis
	1570	1580	1590	1600	
2519	CGCCCGTGACGAATCA-GCGGTACTAACCAACCCAAACCG				M.tuberculosis
1821	CGTCCCGTGATGAATCA-GCGGTACTAACCAACCCAAACCG				M.avium
1821	CGTCCCGTGATGAATCA-GCGGTACTAACCAACCCAAACCG				M.paratuberc.
1915	CGTCCCGTGATGAATCACTATTGACTAACCAACCCAAACCG				M.phlei
1840	CGCCCGTGATGAATCA-GCGGTACTAACCAACCCAAACCG				M.leprae
1602	CGCCCGTGATGAATCA-GCGGTACTAACCAACCCAAACCG				M.gastri
1545	CGCCCGTGATGAATCA-GCGGTACTAACCAACCCAAACCG				M.kansasii
3996	CGTCCCGTGATGAATCA-GCGGTACTAACCAACCCAAACCG				M.smegmatis

Figure 1F

7/31

	1610	1620	1630	1640	
2558	GAT-CGATCAC-TCCCCTTCGGGGG-TGTGGAGTTC-TGG				M. tuberculosis
1860	GAT-CGACCAT-TCCCCTTCGGGGG-GTGGCGATT-TGG				M. avium
1860	GAT-CGACCAT-TCCCCTTCGGGGG-GTGGCGATT-TGG				M. paratuberc.
1955	GCG-CGATC-ATCC-TTCGGGG-GTGGAGGTG-GG				M. phlei
1879	GAT-CGACCAT-TATCCCCTTCGGGGG-TATGGAGGT-TGG				M. leprae
1641	GAT-CGATCAC-TCCCCTTCGGGGG-GTGGAGGTC-TGG				M. gastri
1584	GAT-CGATCAC-TCCCCTTCGGGGG-GTGGAGGTC-TGG				M. kansasii
4035	ACCGTGAGCGACT-TTCGGGG-TGTGGGTGG-TGG				M. smegmatis
	1650	1660	1670	1680	
2594	GGCTCGGTGGGAACCTCGCTGGTAGTAGTCAAAGCGAATGGG				M. tuberculosis
1896	GGCTCGGTGGGAACCTCGCTGGTAGTAGTCAAAGCGAATGGG				M. avium
1896	GGCTCGGTGGGAACCTCGCTGGTAGTAGTCAAAGCGAATGGG				M. paratuberc.
1986	GGCTCGGTGGGAACCG-GTGGTAGTAGTCAAAGCGAATGGG				M. phlei
1917	GGCTCGGTGGGAACCTTCGTTGGTAGTAGTCAAAGCGAATGGG				M. leprae
1677	GGCTCGGTGGAGACCTTCGCTGGTAGTAGTCAAAGCGAATGGG				M. gastri
1620	GGCTCGGTGGAGACCTTCGCTGGTAGTAGTCAAAGCGAATGGG				M. kansasii
4071	GGCTCGGTGGGAACCTTCGTTGGTAGTAGTCAAAGCGAATGGG				M. smegmatis
	1690	1700	1710	1720	
2634	-GTGACCGAGGAAGGTAGCCGTACCAAGTCAGTGGTAATA-				M. tuberculosis
1936	-GTGACCGAGGAAGGTAGCCGTACCAAGTCAGTGGTAATA-				M. avium
1936	-GTGACCGAGGAAGGTAGCCGTACCAAGTCAGTGGTAATA-				M. paratuberc.
2025	-GTGACCGAGGAAGGTAGCCGTACCAAGTCAGTGGTAATA-				M. phlei
1957	-GTGACCGAGGAAGGTAGCCGTACCAAGTCAGTGGTAATA-				M. leprae
1717	-GTGACCGAGGAAGGTAGCCGTACCAAGTCAGTGGTAATA-				M. gastri
1660	-GTGACCGAGGAAGGTAGCCGTACCAAGTCAGTGGTAATA-				M. kansasii
4111	-GTGACCGAGGAAGGTAGCCGTACCGTCAGTGGTAATA-				M. smegmatis

Figure 1G

8/31

	1730	1740	1750	1760	
2672	-CTGGGGCAAGCCGGTAGGGAGAGCGATAGGCAAATCCGT				M. tuberculosis
1974	-CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAATCCGT				M. avium
1974	-CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAATCCGT				M. paratuberc.
2063	-C G GGGG TAA ACCGTAGGGAGAG T ATAGGCAAATCCGT				M. phlei
1995	-CTGG A GAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT				M. leprae
1755	-CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT				M. gastri
1698	-CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT				M. kansasii
4149	-C G GG G TAA AGCC T AGGGAGTCAGATAGG T ATCCGT				M. smegmatis

	1970	1980	1990	2000	
2908	AGGGGG A CCGGAATA T CGTGAACACCCTTGC GG GGC M. tuberculosis				
2208	AGGGGG C CCGGAATA T CGTGAACACCCTTGC GG GGC M. avium				
2208	AGGGGG C CCGGAATA T CGTGAACACCCTTGC GG GGC M. paratuberc.				
2298	AGGGGGACCC A CGTA T CGTGA GGG T CTTGCGG G AGC M. phlei				
2231	AGGGGG C CCGGAATA T CGTGAACACCCTTGC GG GGC M. leprae				
1910					M. gastri
1934	AGGGGGACCGGAATA T CGTGAACACCCTTGC GG GGC M. kansasii				
4385	AGGGGGACCC A CGT GG CGT G T AGCC T ACGG CCC AGC M. smegmatis				

	2410	2420	2430	2440	
3345	AC T CGACGCCAGTTGGGG G GAGTCGTTGAAATACC				M. tuberculosis
284	AC T CGACGCCAGTTGGGG G GAGTCGTTGAAATACC				M. bovis
2645	G ACAGACGCCAGTTGGAGTCGTTGAAATACC				M. avium
393	ATACAGACGCCAGTTGGAGTCGTTGAAATACC				M. intracellulare
2645	G ACAGACGCCAGTTGGAGTCGTTGAAATACC				M. paratuberc.
2737	G TCGGACGCCAGTTGGG G GAGTCGTTGAAATACC				M. phlei
2668	AC T CGACGCCAGTTGGG G GAGTCGTTGAAATACC				M. leprae
1910					M. gastri
2372	ACCTC T ACGCCAGTTGGG G GAGTCGTTGAAATACC				M. kansasii
4822	G TCACACGCCAGTG GGG G GAGTCGTTGAAATACC				M. smegmatis

Figure 1H

9/31

	2450	2460	2470	2480	
3385	ACTCTGATCGTATTGGC	GCATCTAACCTCGAACCCCTGAATC			M. tuberculosis
324	ACTCTGATCGTATTGGGCATCTAACCTCGAACCCCTGAATC				M. bovis
2685	ACTCTGATCGTATTGGCACA	CTAACCTCGAACCCCT-TATC			M. avium
433	ACTCTGATCGTATTGGCACA	CTAACCTCGAACCCCT-TATC			M. intracellulare
2685	ACTCTGATCGTATTGGCACA	CTAACCTCGAACCCCT-TATC			M. paratuberc.
2777	ACTCTGATCGTATTGGCACA	CTAACCTCGAACCCCT-TATC			M. phlei
2708	ACTCTGATCGTATTGGCACA	CTAACCTCGAACCCCT-TATC			M. leprae
1910					M. gastri
2412	ACTCTGATCGTATTGGCACA	CTAACCTCGAACCCCTGAATC			M. kansasii
4862	ACTCTGATCGTATTGGCACA	CTAACCTCGAACCCCT-TATC			M. smegmatis
	2490	2500	2510	2520	
3425	GGGTTTAGGGACAGTGCC	TGGCGGGTAGTTAAC	TGGGGC		M. tuberculosis
364	GGGTTAGGGACAGTGCC	TGGCGGGTAGTTAAC	TGGGGC		M. bovis
2724	GGGTTAGGGACAGTGCC	TGGCGGGTAGTTAAC	TGGGGC		M. avium
472	GGGTTAGGGACAGTGCC	TGGCGGGTAGTTAAC	TGGGGC		M. intracellulare
2724	GGGTTAGGGACAGTGCC	TGGCGGGTAGTTAAC	TGGGGC		M. paratuberc.
2817	GGGTTAGGGACAGTGCC	TGGGTAGTTAAC	TGGGGC		M. phlei
2748	GGGTTAGGGACAGTGCC	TGGGTAGTTAAC	TGGGGC		M. leprae
1910					M. gastri
2452	GGGTTAGGGACAGTGCC	TGGGTAGTTAAC	TGGGGC		M. kansasii
4902	GGGTTAGGGACAGTGCC	TGGGTAGTTAAC	TGGGGC		M. smegmatis

	2930	2940	2950	2960	
3864	AGTACGAGAGGACCGGGACGGACGA	ACCCCTCTGGTGACCA			M. tuberculosis
3163	AGTACGAGAGGACCGGGACGGACGA	ACCCCTCTGGTATACCA			M. avium
3163	AGTACGAGAGGACCGGGACGGACGA	ACCCCTCTGGTATACCA			M. paratuberc.
3256	AGTACGAGAGGACCGGGACGGACGA	ACCCCTCTGGTATACCA			M. phlei
3187	AGTACGAGAGGACCGGGACGGACGA	ACCCCTCTGGTATACCA			M. leprae
1910					M. gastri
2891	AGTACGAGAGGACCGGGACGGACGA	ACCCCTCTGGTATACCA			M. kansasii
5342	AGTACGAGAGGACCGGGACGGACGA	ACCCCTCTGGTATACCA			M. smegmatis

Figure 1I

10/31

	2970	2980	2990	3000	
3904	GTTGTCCC	CCAGGGGCACCGCTGGATAGCCACGTTGGT			M. tuberculosis
3203	GTTGTCCC	CCAGGGGCACCGCTGGATAGCCACGTTGGA			M. avium
3203	GTTGTCCC	CCAGGGGCACCGCTGGATAGCCACGTTGGA			M. paratuberc.
3296	GTTGTCCC	CCAGGGGCACCGCTGGATAGCCACGTTGGA			M. phlei
3227	GTTGTCCC	CCAGGGGCACCGCTGGATAGCCACGTTGGA			M. leprae
1910					M. gastri
2931	GTTGTCCC	CCAGGGGCACCGCTGGATAGCCACGTTGGA			M. kansasii
5382	GTTGTCCC	CCAGGGGCACCGCTGGATAGCCACGTTGGA			M. smegmatis

	3010	3020	3030	3040	
3944	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M. tuberculosis
3243	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M. avium
3243	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M. paratuberc.
3336	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M. phlei
3267	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M. leprae
1910					M. gastri
2971	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M. kansasii
5422	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M. smegmatis

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	3090	3100	3110	3120	
4023	CCCGC-AGAACACGGG	TTCATAGGT	CAGACCTGGAAAGCT		M. tuberculosis
609	CCCGC-AGAACACGGG	TTCAATAGGT	CAGACCTGGAAAGCT		M. bovis
3322	CCCGC-AGAACACGGG	TTGATAGG	CAGACCTGGAAAGCT		M. avium
677	CCCGC-AGAACACGGG	TTGATAGG	CAGACCTGGAAAGCT		M. intracellulare
3322	CCCGC-AGATCACGGG	TTGATAGG	CAGACCTGGAAAGCT		M. paratuberc.
3415	CCCGC-AGAACACGGG	TTGATAGG	CAGACCTGGAAAGCT		M. phlei
3309					M. leprae
1910					M. gastri
3050	CCCGC-AGAACACGGG	TTGATAGG	CAGACCTGGAAAGCT		M. kansasii
5501	CCCGC-AGAACACGGG	TTGATAGG	CAGACCTGGAAAGCT		M. smegmatis

Figure 1J

	50	60	70	80	
2	GC	GGCGTGTCTAA	CACATGCAAGTCGAACCGGAAAG	GTC T	M. tuberculosis
141	GC	GGCGTGTCTAA	CACATGCAAGTCGAACCGGAAAGG	T CTC	M. bovis
39	GC	GGCGTGTCTAA	CACATGCAAGTCGAACCGGAAAGG	T CTC	M. avium
1	-----	TTAACACATGCAAGT	GAACCGGAAAGG	T CTC	M. intracellulare
39	GC	GGCGTGTCTAA	CACATGCAAGTCGAACCGGAAAGG	T CTC	M. paratuberc.
2	GC	GGCGTGTCTAA	CACATGCAAGTCGAACCGGAAAGG	T CTC	M. scrofulaceum
40	GC	GGCGTGTCTAA	CACATGCAAGTCGAACCGGAAAGG	T CTC	M. leprae
2	GC	GGCGTGTCTAA	CACATGCAAGTCGAACCGGAAAGG	T CTC	M. kansasii
2	GC	GGCGTGTCTAA	CACATGCAAGTCGAACCGGAAAGG	T CTC	M. gastri
40	GC	GGCGTGTCTAA	CACATGCAAGTCGAACCGGAAAGG	T CTC	M. gordonae
1	-----	GTGCTTAACACATGCAAGTCGAACCGGAAAGG	T CTC	M. marinum	

	90	100	110	120	
42	T-----	TCGG	A GATACTCGAGTGGCGAACGGGT	M. tuberculosis	
181	T-----	TCGGAGATACTCGAGTGGCGAACGGGT	M. bovis		
79	T-----	TCGGAGGTACTCGAGTGGCGAACGGGT	M. avium		
32	T-----	TCGGGGTACTCGAGTGGCGAACGGGT	M. intracellulare		
79	T-----	TCGGAGGTACTCGAGTGGCGAACGGGT	M. paratuberc.		
42	T-----	TCGGGGTACTCGAGTGGCGAACGGGT	M. scrofulaceum		
80	TAAAAAAATCTTT	TTAGAGATACTCGAGTGGCGAACGGGT	M. leprae		
41	T-----	TCGGAGA	ACTCGAGTGGCGAACGGGT	M. kansasii	
42	T-----	TCGGAGA	ACTCGAGTGGCGAACGGGT	M. gastri	
80	-----	GGGTAC	ACTCGAGTGGCGAACGGGT	M. gordonae	
36	T-----	TCGGAGATACTCGA	ATGGCGAACGGGT	M. marinum	

	130	140	150	160	
70	GAGTAACACGTGGG	T CATCTGCCCTGCAC	TC-GGGATAA	M. tuberculosis	
209	GAGTAACACGTGGG	GATCTGCCCTGCAC	TC-GGGATAA	M. bovis	
107	GAGTAACACGTGGG	CAATCTGCCCTGCAC	TC-GGGATAA	M. avium	
59	GAGTAACACGTGGG	CAATCTGCCCTGCAC	TC-GGGATAA	M. intracellulare	
107	GAGTAACACGTGGG	CAATCTGCCCTGCAC	TC-GGGATAA	M. paratuberc.	
70	GAGTAACACGTGGG	CAATCTGCCCTGCAC	TC-GGGATAA	M. scrofulaceum	
120	GAGTAACACGTGGG	CAATCTGCCCTGCAC	TC-GGGATAA	M. leprae	
69	GAGTAACACGTGGG	CAATCTGCCCTGCAC	TC-GGGATAA	M. kansasii	
70	GAGTAACACGTGGG	CAATCTGCCCTGCAC	TC-GGGATAA	M. gastri	
104	GAGTAACACGTGGG	CAATCTGCCCTGCAC	TC-GGGATAA	M. gordonae	
64	GAGTAACACGTGGG	CAATCTGCCCTGCAC	TC-GGGATAA	M. marinum	

Figure 2A

12/31

	170	180	190	200	
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M. tuberculosis
248	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M. bovis
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M. avium
98	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTGGAT				M. intracellulare
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M. paratuberc.
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M. scrofulaceum
160	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M. leprae
108	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M. kansasii
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M. gastri
143	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M. gordonae
103	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M. marinum
	210	220	230	240	
149	TGCATGCTTGTTGGGAAAGCGCTTTAGCGGGTGTGGGAT				M. tuberculosis
288	TGCATGCTTGTTGGTGGAAAGCGCTTTAGCGGGTGTGGGAT				M. bovis
186	TGCATGCTTGTTGGTGGAAAGC-TTTTACGGGTGTGGGAT				M. avium
138	TGCATGCTTGTTGGTGGAAAGC-TTTTACGGGTGTGGGAT				M. intracellulare
186	TGCATGCTTGTTGGTGGAAAGC-TTTTACGGGTGTGGGAT				M. paratuberc.
149	TGCATGCTTGTTGGTGGAAAGC-TTTTACGGGTGTGGGAT				M. scrofulaceum
200	TGCATGCTTGTTGGTGGAAAGC-TTTTACGGGTGTGGGAT				M. leprae
148	TGCATGCTTGTTGGTGGAAAGC-TTTTACGGGTGTGGGAT				M. kansasii
149	TGCATGCTTGTTGGTGGAAAGC-TTTTACGGGTGTGGGAT				M. gastri
183	TGCATGCTTGTTGGTGGAAAGC-TTTTACGGGTGTGGGAT				M. gordonae
143	TGCATGCTTGTTGGTGGAAAGC-TTTTACGGGTGTGGGAT				M. marinum
	250	260	270	280	
189	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. tuberculosis
328	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. bovis
224	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. avium
176	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. intracellulare
224	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. paratuberc.
187	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. scrofulaceum
239	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. leprae
186	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. kansasii
187	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. gastri
221	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. gordonae
181	GAGCCCGCGGCCCTATCAGCTTGGTGGGTGACGGCCT				M. marinum

Figure 2B

13/31

	450	460	470	480	
389	AAACCTCTTCACCATCGACGAAGGTCCCCGGTT	CTCTCGG	M.tuberculosis		
528	AAACCTCTTCACCATCGACGAAGGTCCCCGGTT	CTCTCGG	M.bovis		
424	AAACCTCTTCACCATCGACGAAGGTCCCCGGTT	CTCTCGG	M.avium		
376	AAACCTCTTCACCATCGACGAAGGTCCCCGGTT	CTCTCGG	M.intracellulare		
424	AAACCTCTTCACCATCGACGAAGGTCCCCGGTT	CTCTCGG	M.paratuberc.		
387	AAACCTCTTCACCATCGACGAAGGT	CTCA---CTTG	GGG M.scrofulaceum		
439	AAACCTCTTCACCATCGACGAAGGT	CTGGG	CTTCTCGG M.leprae		
386	AAACCTCTTCACCATCGACGAAGGT	CTGGG	CTTCTCGG M.kansasii		
387	AAACCTCTTCACCATCGACGAAGGT	CTGGG	CTTCTCGG M.gastri		
420	AAACCTCTTCACCATCGACGAAGGT	CTGGG	CTTCTCGG M.gordonae		
381	AAACCTCTTCACCATCGACGAAGGT	CTGGG	CTTCTCGG M.marinum		

	1130	1140	1150	1160	
1069	TCTCATGTTGCCAGC	ACGTAATGGT	GGGACTCGTGAGAG		M.tuberculosis
1208	TCTCATGTTGCCAGC	ACGTAATGGT	GGGACTCGTGAGAG		M.bovis
1104	TCTCATGTTGCCAGC	GGGTAATG	GGGGACTCGTGAGAG		M.avium
1056	TCTCATGTTGCCAGC	GGGTAATG	GGGGACTCGTGAGAG		M.intracellulare
1098	TCTCATGTTGCCAGC	GGGTAATG	GGGGACTCGTGAGAG		M.paratuberc.
1064	TCTCATGTTGCCAGC	GGGTAATG	GGGGACTCGTGAGAG		M.scrofulacéum
1119	TCTCATGTTGCCAGC	ACGTAATGGT	GGGGACTCGTGAGAG		M.leprae
1066	TCTCATGTTGCCAGC	GGGTAATG	GGGGACTCGTGAGAG		M.kansasii
1067	TCTCATGTTGCCAGC	GGGTAATG	GGGGACTCGTGAGAG		M.gastri
1100	TCTCATGTTGCCAGC	GGGTAATG	GGGGACTCGTGAGAG		M.gordonae
1061	TCTCATGTTGCCAGC	ACGTAATGGT	GGGGACTCGTGAGAG		M.marinum

	1250	1260	1270	1280	
1189	CAATGCCGGTACA	AAAGGGCTGCATGCCG	CGAGGTTAAG		M.tuberculosis
1328	CAATGCCGGTACA	AAAGGGCTGCATGCCG	CGAGGTTAAG		M.bovis
1224	CAATGCCGGTACA	AAAGGGCTGCATGCCG	TAAGGTTAAG		M.avium
1176	CAATGCCGGTACA	AAAGGGCTGCATGCCG	TAAGGTTAAG		M.intracellulare
1218	CAATGCCGGTACA	AAAGGGCTGCATGCCG	TAAGGTTAAG		M.paratuberc.
1184	CAATGCCGGTACA	AAAGGGCTGCATGCCG	TAAGGTTAAG		M.scrofulaceum
1239	CAATGCCGGTACA	AAAGGGCTGCATGCCG	TAAGGTTAAG		M.leprae
1186	CAATGCCGGTACA	AAAGGGCTGCATGCCG	CGAGGTTAAG		M.kansasii
1187	CAATGCCGGTACA	AAAGGGCTGCATGCCG	CGAGGTTAAG		M.gastri
1220	CAATGCCGGTACA	AAAGGGCTGCATGCCG	CGAGGTTAAG		M.gordonae
1181	CAATGCCGGTACA	AAAGGGCTGCATGCCG	CGAGGTTAAG		M.marinum

Figure 2C

	1290	1300	1310	1320	
1229	CGAATCCTTA-A	AAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.tuberculosis	
1368	CGAATCCTTA-AAAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.bovis		
1264	CGAATCCTTAAAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.avium		
1216	CGAATCCTTTAAAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.intracellulare		
1258	CGAATCCTTTAAAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.paratuberc.		
1224	CGAATCCTTTAAAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.scrofulaceum		
1279	CGAATCCTTTAAAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.leprae		
1226	CGAATCCTTTAAAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.kansasii		
1227	CGAATCCTTTAAAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.gastri		
1260	CGAATCCTTTAAAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.gordonae		
1221	CGAATCCTTAAAGCCGGTCTCAGTTGGGAT	CGGGTCT	M.marinum		
	1330	1340	1350	1360	
1268	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.tuberculosis			
1407	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.bovis			
1304	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.avium			
1256	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.intracellulare			
1298	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.paratuberc.			
1264	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.scrofulaceum			
1319	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.leprae			
1266	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.kansasii			
1267	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.gastri			
1300	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.gordonae			
1260	GCAACTCGACCCCCGTGAAGTCGGAGTCGGTAGTAATCGCA	M.marinum			

Figure 2D

	50	60	70	80	
128	TTCCGAACCGGGAGCTAAGCCTGCCAGCGCGATGATAC				M. tuberculosis
39	TGCCGAACCGGGAGCTAAGCCTGCCAGCGCGATGATAC				M. bovis
41	TCGGAAACCGGGAGCTAAGCCTGCCAGCGCGATGATAC				M. phlei
3559	TACCGAACCGGGAGCTAAGCCTG[CAGCGCGATGATAC]				M. leprae
5743	TGCCGAACCGGGAGCTAAGCCTGCCAGC[CCGATGATAC]				M. smegmatis

	90	100	110	120	
168	TGCCCTTCCC[G---TGGAAAAGTAGGACACCGCGGAAC				M. tuberculosis
79	TGCCCTTCCC[G---TGGAAAAGTAGG[CACCGCGGAAC				M. bovis
81	TGCCCTTCA[G---TGGAAAAGTAGGACACCGCGGAAC				M. phlei
3599	TGCCCTTICGGG---TGGAAAAGTAGGACAC[GCGGAAC				M. leprae
5782	TACCCCTT[G---TGGAAAAGTAGGACACCGCGGAAC				M. smegmatis

Figure 3

16/31

	90	100	110	120	
382	GGGAGCTGTCAACCGAGC	AT	GATCCGAGGATTCCGAAT		M. avium
382	GGGAGCTGTCAACCGAGC	AT	GATCCGAGGATTCCGAAT		M. paratuberc.
1053	GGGAGCTGTCAACCGAGC	GG	GATCCGAGGATTCCGAAT		M. tuberculosis
467	GGGAGCTGTCAACCGAGC	GG	GATCCGAGGATTCCGAAT		M. phlei
392	GGGAGCTGTCAACCGAGC	GG	GATCCGAGGATTCCGAAT		M. leprae
167	GGGAGCTGTCAACCGAGC	GG	GATCCGAGGATTCCGAAT		M. gastri
110	GGGAGCTGTCAACCGAGC	GG	GATCCGAGGATTCCGAAT		M. kansasii
2548	GGGAGCTGTCAACCGAGC	GG	GATCCGAGGAT	CCGAAT	M. smegmatis

	170	180	190	200	
462	GAATATATAAGGGTGC	GGAGG	AACGCCGGAAAGTGAAA		M. avium
462	GAATATATAAGGGTGC	GGAGG	AACGCCGGAAAGTGAAA		M. paratuberc.
1133	GAATATATAAGGGTGC	GGAGG	AACGCCGGAAAGTGAAA		M. tuberculosis
547	GAATATATAAGG	CGT	GGGGAAACGCCGGAAAGTGAAA		M. phlei
472	GAATATATAAGG	T	GGGGAAACGCCGGAAAGTGAAA		M. leprae
247	GAATATATAAGGGTGC	GGAGG	AACGCCGGAAAGTGAAA		M. gastri
190	GAATATATAAGGGTGC	GGAGG	AACGCCGGAAAGTGAAA		M. kansasii
2628	GAATATATAAGG	CGT	GGGGAAACGCCGGAAAGTGAAA		M. smegmatis

	250	260	270	280	
541	-GTCAGTAGTGGCGAGCGA	C	CGGAACA-GGCTAAACCG		M. avium
541	-GTCAGTAGTGGCGAGCGA	C	CGGAACA-GGCTAAACCG		M. paratuberc.
1212	-GCAAGTAGTGGCGAGCGA	C	CGGAACA-GGCTAAACCG		M. tuberculosis
626	-GTGAGTAGTGGCGAGCGA	A	AGGGAGGAGGGCTAAACCG		M. phlei
551	-GCAAGTAGTGGCGAGCGA	A	AGGGAGGAGGGCTAAACCG		M. leprae
326	-GTCAGTAGTGGCGAGCGA	A	CGGAACATGGCTAAACCG		M. gastri
269	-GTAAGTAGTGGCGAGCGA	A	CGGAACATGGCTAAACCG		M. kansasii
2706	-GTCAGTAGTGGCGAGCGA	A	CGGAAGGAGGGCTAAACCG		M. smegmatis

Figure 4A

17/31

	290	300	310	320	
578	CATG-CATG[GACAACC]GGGTAGGGGTTGTGTGC[G]GGGT				M. avium
578	CATG-CATGGACAACC[G]GGTAGGGGTTGTGTGC[G]GGGT				M. paratuberc.
1250	CA[G]-CATGGCTAACCGGGTAGGGGTTGTGTGC[G]GGGT				M. tuberculosis
664	C[G]TG-CATGTGATAACCGGGT[G]GGGTAGGGGTTGTGTGC[G]GGGT				M. phlei
590	CACA-CATGTCTAACACTAGGTAGGGGTTGTGTGC[G]GGGT				M. leprae
365	CA[G]-CATGGGTGACCGGGTAGGGGTTGTGTGC[G]GGGT				M. gastri
308	CA[G]-CATGGGTGACCGGGTAGGGGTTGTGTGC[G]GGGT				M. kansasii
2745	[ATG]ACATGTGATAACCGGGTAGGGGTTGTGTGC[G]GGGT				M. smegmatis

	330	340	350	360	
617	TGTGGATTGATATGTCAGCTCACCTGGCTGAGG-GG				M. avium
617	TGTGGGATTGATATGTCAGCTCACCTGGCTGAGG-GG				M. paratuberc.
1289	TGTGGGAG-GATATGTCAGCTCACCTGGCTGAGG-GG				M. tuberculosis
703	TGTGGG[G]CTGTGTC[G]CATCGTCCG[G]GGC[G]ATGGC[G]AG				M. phlei
629	TGTGGGATTGATATGTCAGCTCACCTGGCTGAGG-GG				M. leprae
404	TGTGGGAT[G]ATA[G]TCTCAGCTCACCTGGCTGAGG-GG				M. gastri
347	TGTGGGAT[G]ATA[G]TCTCAGCTCACCTGGCTGAGG-GG				M. kansasii
2785	TGTGGGACCTATGTC[G]CTCACCTGGCTG[G]AGGG				M. smegmatis

	370	380	390	400	
656	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAC				M. avium
656	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAC				M. paratuberc.
1327	[AGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAC]				M. tuberculosis
742	TA[G]TAAAG[CAG]TG[G]GGTAG[G]AAGTGGCCTGGGAT				M. phlei
668	TA[G]TCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M. leprae
443	[AGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT]				M. gastri
386	[AGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT]				M. kansasii
2823	[AGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT]				M. smegmatis

Figure 4B

18/31

	410	420	430	440	
696	GGCCC <u>C</u> CGTAGACGGTGAGAGCCCCGGTACCGCGAAA-ACC				M. avium
696	GGCCCGCCGTA <u>G</u> ACGGTGAGAGCCCCGGTACCGCGAAA-ACC				M. paratuberc.
1367	GGTC <u>T</u> GCCGTAGACGGTGAGAGCCCCGGTACCGCGAAA-ACC				M. tuberculosis
782	GGTC <u>T</u> GCCGTAG <u>T</u> GGTGAGAGCCCCGGTACCGCGAAA-ACC				M. phlei
708	GGCC <u>T</u> GCCGTAGACGGTGAGAGCCCCGGTACCGCGAAA-ACC				M. leprae
483	GGTC <u>T</u> GCCGTAGACGGTGAGAGCCCCGGTACCGTGAAA-ACC				M. gastri
426	GGTC <u>T</u> GCCGTAGACGGTGAGAGCCCCGGTACCGTGAAA-ACC				M. kansasii
2863	GGCC <u>T</u> CCGTAGACGGTGAGAGCCCCGGTACCGTGAAA-ACC				M. smegmatis
	450	460	470	480	
735	CGGCACCTGCCT <u>T</u> ATATCAAC <u>A</u> CCGAGTAGCAGCGGGCC				M. avium
735	CGGCACCTGCCT <u>T</u> ATATCAAC <u>A</u> CCGAGTAGCAGCGGGCC				M. paratuberc.
1406	CGGCACCTGCCT <u>T</u> ATCA <u>A</u> TTCCCGAGTAGCAGCGGGCC				M. tuberculosis
820	CG <u>T</u> GC <u>T</u> GG <u>T</u> GTACAGG--TCCCGAGTAGCAGCGGGCC				M. phlei
747	CGGCACCTGCCT <u>T</u> ATCA <u>A</u> TTCCCGAGTAGCAGCGGGCC				M. leprae
522	CGGCACCTGCCT <u>T</u> ATCA <u>A</u> TTCCCGAGTAGCAGCGGGCC				M. gastri
465	CGGCACCTGCCT <u>T</u> ATCA <u>A</u> TTCCCGAGTAGCAGCGGGCC				M. kansasii
2902	CG <u>A</u> CG <u>T</u> GT <u>T</u> ATGGTGT <u>T</u> CCCGAGTAGCAGCGGGCC				M. smegmatis
	570	580	590	600	
855	GAGGGAA <u>T</u> GGT <u>A</u> AAAGTACCCCGGG <u>AGGG</u> -AGTGA <u>AATA</u>				M. avium
855	GAGGGAA <u>T</u> GGT <u>A</u> AAAGTACCCCGGG <u>AGGG</u> -AGTGA <u>AATA</u>				M. paratuberc.
1526	GAGGGAA <u>T</u> GGT <u>A</u> AAAGTACCCCGGG <u>AGGG</u> -AGTGA <u>AATA</u>				M. tuberculosis
937	GAGGGAA <u>T</u> GGT <u>A</u> AAAGTACCCCGGG <u>AGGG</u> -AGTGA <u>AAGA</u>				M. phlei
867	GAGGGAA <u>T</u> GGT <u>A</u> AAAGTACCCCGGG <u>AGGG</u> -AGTGA <u>AATA</u>				M. leprae
642	GAGGGAA <u>T</u> GGT <u>A</u> AAAGTACCCCGGG <u>AGGG</u> -AGTGA <u>AAGA</u>				M. gastri
585	GAGGGAA <u>T</u> GGT <u>A</u> AAAGTACCCCGGG <u>AGGG</u> -AGTGA <u>AAGA</u>				M. kansasii
3022	GAGGGAA <u>T</u> GGT <u>A</u> AAAGTACCCCGGG <u>AGGG</u> -AGTGA <u>AAGA</u>				M. smegmatis

Figure 4C

	610	620	630	640	
894	GTACCTGAAACC GTGTGCCTACAATCCGTCAAGAGCCT	TCCT	M. avium		
894	GTACCTGAAACC GTGTGCCTACAATCCGTCAAGAGCCT	CCCT	M. paratuberc.		
1566	GTACCTGAAACC GTGTGCCTACAATCCGTCAAGAGCCT	CCCT	M. tuberculosis		
976	GTACCTGAAACC GTGTGCCTACAATCCGTCAAGAGCCT	CCCT	M. phlei		
907	GTACCTGAAACC GTGTGCCTACAATCCGTCAAGAGCCT	CCCT	M. leprae		
682	GTACCTGAAACC GTGTGCCTACAATCCGTCAAGAGCCT	CCCT	M. gastri		
625	GTACCTGAAACC GTGTGCCTACAATCCGTCAAGAGCCT	CCCT	M. kansasii		
3062	GTACCTGAAACC GTGTGCCTACAATCCGTCAAGAGCCT	CCCT	M. smegmatis		
	650	660	670	680	
934	C-----	GTGGGGTGTATGGCGTGCCCTTTGA	M. avium		
934	C-----	GTGGGGTGTATGGCGTGCCCTTTGA	M. paratuberc.		
1606	TTT CCTCT CCGGGAGGAC	GTGGGTGTATGGCGTGCCCTTTGA	M. tuberculosis		
1016	CTT-----	GTGGGGTGTATGGCGTGCCCTTTGA	M. phlei		
947	T-----	GTGGGGTGTATGGCGTGCCCTTTGA	M. leprae		
722	T-----	GTGGGGTGTATGGCGTGCCCTTTGA	M. gastri		
665	C-----	GTGGGGTGTATGGCGTGCCCTTTGA	M. kansasii		
3102	ACGTGT-----	GTGGGGTGTATGGCGTGCCCTTTGA	M. smegmatis		
	690	700	710	720	
959	AGAATGAGCCTGCGAGTCAGGGT	CACGT CGCGAGGTTAAC	M. avium		
23	AGAATGAGCCTGCGAGTCAGGGAC	AGCTCGCGAGGTTAAC	M. intracellulare		
959	AGAATGAGCCTGCGAGTCAGGGAC	AGCTCGCGAGGTTAAC	M. paratuberc.		
646	AGAATGAGCCTGCGAGTCAGGGAC	AGCTCGCGAGGTTAAC	M. tuberculosis		
1	AGAATGAGCCTGCGAGTCAGGGAC	AGCTCGCGAGGTTAAC	M. bovis		
046	AGAATGAGCCTGCGAGTCAGGGAC	AGCTCGCGAGGTTAAC	M. phlei		
72	AGAATGAGCCTGCGAGTCAGGGAC	AGCTCGCGAGGTTAAC	M. leprae		
747	AGAATGAGCCTGCGAGTCAGGGAC	AGCTCGCGAGGTTAAC	M. gastri		
590	AGAATGAGCCTGCGAGTCAGGGAC	AGCTCGCGAGGTTAAC	M. kansasii		
1132	AGAATGAGCCTGCGAGTCAGGGAC	AGCTCGCGAGGTTAAC	M. smegmatis		

Figure 4D

20/31

	770	780	790	800	
1039	CGCATCCCTTGGG-----		GTCAGTAGTGGCGTGT		M. avium
103	CGCATCCCTTGGG-----		GTGTAGTGGCGTGT		M. intracellulare
1039	CGCATCCCTTGGG-----		GTGTAGTGGCGTGT		M. paratuberc.
1726	CGACCCACCGCGATACCGCGTGTG-----		GTGTAGTGGCGTGT		M. tuberculosis
84	CGACCCACCGCGATACCGCGTGTG-----		GTGTAGTGGCGTGT		M. bovis
1126	CGTATCCAACCTGTT-----		GGGGTTGGTGTAGTGG-----		M. phlei
1052	CGTATCAGCTGAGCGT-----		GTGTAGTGGCGTGT		M. leprae
827	CGTATCAGCGTAAGCGT-----		GTGTAGTGGCGTGT		M. gastri
770	CGTATCCCGCGAGCGT-----		GTGTAGTGGCGTGT		M. kansasii
3212	CGTATCCACAAAGAGGTGTG-----		GTGTAGTGGGTGT		M. smegmatis

	1050	1060	1070	1080	
1307	CAGCCAAACTCCGAATGCCG-----	TGGTG-TAAAAGCGTGGCA			M. avium
1307	CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA-----				M. paratuberc.
2005	CAGCCAAACTCCGAATGCCG-TGGTG-TA-----	AAGCGTGGCA			M. tuberculosis
1401	CAGCCAAACTCCGAATGCCGATAAG-----	TAAAAGCGTGGCA			M. phlei
1323	CAGCCAAACTCCGAATGCCG-TGGTG-----	TAAAAGCGTGGCA			M. leprae
1098	CAGCCAAACTCCGAATGCCG-TGGTG-TATA-----	GCCTGGCA			M. gastri
1041	CAGCCAAACTCCGAATGCCG-TGGTG-TATA-----	GCCTGGCA			M. kansasii
3486	CAGCCAAACTCCGAATGCCGATAAGCGAAAGCGGG-----	A			M. smegmatis

	1170	1180	1190	1200	
1425	AGTGGAAAAGGATGTCTAGTCGCAAGA-GACAACCAGGAGG				M. avium
1425	AGTGGAAAAGGATGTCTAGTCGCAAGA-GACAACCAGGAGG				M. paratuberc.
2122	AGTGGAAAAGGATGTCTAGTCGCAAGA-GACAACCAGGAGG				M. tuberculosis
1519	AGTGGAAAAGGATGTCTAGTCGCAAGA-GACAACCAGGAGG				M. phlei
1441	AGTGGAAAAGGATGTCTAGTCGCAAGA-GACAACCAGGAGG				M. leprae
1215	AGTGGAAAAGGATGTCTAGTCGCAAGA-GACAACCAGGAGG				M. gastri
1158	AGTGGAAAAGGATGTCTAGTCGCAAGA-GACAACCAGGAGG				M. kansasii
3606	AGTGGAAAAGGATGTCTAGTCGCAAGA-GACAACCAGGAGG				M. smegmatis

Figure 4E

	1250	1260	1270	1280	
1504	CTCACTGGTCAAGTGATT	ATGCCCGATAATGTAGC	GGGG		M. avium
1504	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGC	GGGG		M. paratuberc.
2201	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGC	GGGG		M. tuberculosis
1598	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGC	GGGG		M. phlei
1520	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGC	GGGG		M. leprae
1294	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGC	GGGG		M. gastri
1237	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGC	GGGG		M. kansasii
3686	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGC	GGGG		M. smegmatis
	1290	1300	1310	1320	
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M. avium
1544	CTCAAGCACACCGCCGAAGCCGCGGCACATT	TCATCTT-TA			M. paratuberc.
2241	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCACCTTG			M. tuberculosis
1638	CTCAAGCACACCGCCGAAGCCGCGGCACAT	-ATCAGCTT	TG		M. phlei
1560	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCACCT	TGTA		M. leprae
1334	CTCAAGCACACCGCCGAAGCCGCGACA	---ACCGC	-TA		M. gastri
1277	CTCAAGCACACCGCCGAAGCCGCGACA	---ACCGC	-TA		M. kansasii
3726	CTCAAGCACACCGCCGAAGCCGCGACA	-GCA	CTT	TG	M. smegmatis
	1330	1340	1350	1360	
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATT	CAGCGAAG	M. avium
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATT	CAGCGAAG	M. paratuberc.
2280	GGTGGATGTGGGTAGGGGAGCGT	CCC	CATT	CAGCGAAG	M. tuberculosis
1676	GGGTGGATGTGGGTAGGGGAGCGT	CCC	CATT	CAGCGAAG	M. phlei
1600	GGGTGGATGTGGGTAGGGGAGCGT	CCC	CATT	CAGCGAAG	M. leprae
1367	GGGT	----TGGGTAGGGGAGCGT	CCC	CATT	CAGCGAAG M. gastri
1310	GGGT	----TGGGTAGGGGAGCGT	CCC	CATT	CAGCGAAG M. kansasii
3764	TT	----TGGGTAGGGGAGCGT	CCC	ATCGCG	GAAAG M. smegmatis

Figure 4F

22/31

	1370	1380	1390	1400
1623	CT-CG GGGTGACCGGTGGTGGAGGGTGGGGGACTGAGAAT			M. avium
1623	CT-CCGGGTGA T CGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. paratuberc.
2319	CCAC CGGGTGACCGGTGGTGGAGGGTGGGGAGTGAGAAT			M. tuberculosis
1716	CCGCCG A GTGA T CGGTGGTGGAGGGTG G GGAGTGAGAAT			M. phlei
1640	CCTCCGGGT A CCGGTGGTGGAGGGTG G GGAGTGAGAAT			M. leprae
1402	CGGCCGGTGACCGGTGGTGGAGGGTG G GGAGTGAGAAT			M. gastri
1345	CTGCCGGTGACCGGTGGTGGAGGGTG G GGAGTGAGAAT			M. kansasii
3796	CGGCCG A GT T CGA T GGTGGAGGGTG G GGAGTGAGAAT			M. smegmatis

	1530	1540	1550	1560
1781	CGATGGACAACGGGTTGATATTCCCGTACCCGT T ATGGG			M. avium
1781	CGATGGACAACGGGTTGATATTCCCGTACCCGT T ATGGG			M. paratuberc.
2479	CGATGGACAACGGGTTGATATTCCCGTACCCGT T ATGGG			M. tuberculosis
1875	CGATGGACAACGGGTTGATATTCCCGTACCCGT T ATGGG			M. phlei
1800	CGATGGACAACGGGTTGATATTCCCGTACCCGT T ATGGG			M. leprae
1562	CGATGGACAACGGGTTGATATTCCCGTACCCGT T ATGGG			M. gastri
1505	CGATGGACAACGGGTTGATATTCCCGTACCCGT T ATGGG			M. kansasii
3956	CGATGGACAACGGGTTGATATTCCCGTACCCGT T ATGGG			M. smegmatis

	1570	1580	1590	1600
1821	CGTCCC TGAT G AATCA-GCGGTACTAACCAACCCAAAACCG			M. avium
1821	CGTCCC T GAT G AATCA-GCGGTACTAACCAACCCAAAACCG			M. paratuberc.
2519	CG CCCC TGAT G AATCA-GCGGTACTAACCAACCCAAAACCG			M. tuberculosis
1915	CGTCCC T GAT G AAT C ATT T TG C TAACCAACCCAAAACCG			M. phlei
1840	CG CCCC TGAT G AATCA-GCGGTACTAACCAACCCAAAACCG			M. leprae
1602	CG CCCC TGAT G AATCA-GCGGTACTAACCAACCCAAAACCG			M. gastri
1545	CG CCCC TGAT G AATCA-GCGGTACTAACCAACCCAAAACCG			M. kansasii
3996	CGTCCC T GAT G AATCA-GCGGTACTAACCAACCCAAAACCG			M. smegmatis

Figure 4G

23/31

	1610	1620	1630	1640	
1860	GAT-CGACCAT-TCCCCCTTCGGGGGC	C-GTGGCGATT-CGG	M. avium		
1860	GAT-CGACCAT-TCCCCCTTCGGGGGC	-GTGGCGATT-CGG	M. paratuberc.		
2558	GAT-CGATCAG-TCCCCCTTCGGGGGC	-TGTGGAGGTG	TGG	M. tuberculosis	
1955	GCG-CGATCAG-TCCCGGGG	-GTGAGGGT	GG	M. phlei	
1879	GAT-CGACCAT-TCCCCCTTCGGGGGC	TATGGAGGT	CGG	M. leprae	
1641	GAT-CGATCAG-TCCCCCTTCGGGGGC	-GTGGAGGT	TGG	M. gastri	
1584	GAT-CGATCAG-TCCCCCTTCGGGGGC	-GTGGAGGT	TGG	M. kansasii	
4035	ACCGTGACCGACGCTT	-TTCGGGC	TGTGGCG	TGGTGG	M. smegmatis
	1650	1660	1670	1680	
1896	GGCTGCGTGC	GACCTTCG	TGGTAGTAGTCAGCAAGC	AAT	GGG M. avium
1896	GGCTGCGTGGGAC	CTTCGCTGGTAGTAGTCAGCAAGC	AAT	GGG M. paratuberc.	
2594	GGCTGCGTGGGA	ACTTCGCTGGTAGTAGTCAGCAAGC	AAT	GGG M. tuberculosis	
1986	GGCTGCGTGGGACCG	-GTGGGTAGTAGTCAGCAAGC	GAT	GGG M. phlei	
1917	GGCTGCGTGGGA	ACTTCG	TGGTAGTAGTCAGCAAGC	GAT	GGG M. leprae
1677	GGCTGCGTGG	AGCCTTCGCTGGTAGTAGTCAGCAAGC	GAT	GGG M. gastri	
1620	GGCTGCGTGG	AGCCTTCGCTGGTAGTAGTCAGCAAGC	GAT	GGG M. kansasii	
4071	GGCTGCA	TGGGACCTTCG	TGGTAGTAGTCAGCAAGC	GAT	GGG M. smegmatis
	1690	1700	1710	1720	
1936	-GTGACGCAGGAAGGCAGCCGTACCA	GTAGTCAGTGGTAATA-			M. avium
1936	-GTGACGCAGGAAGGCAGCCGTACCA	GTAGTCAGTGGTAATA-			M. paratuberc.
2634	-GTGACGCAGGAAGGTAGCCGTACCA	GTAGTCAGTGGTAATA-			M. tuberculosis
2025	-GTGACGCAGGAAGGTAGCCGTACCA	GTAGTCAGTGGTAATA-			M. phlei
1957	-GTGACGCAGGAAGGTAGCCGTACCA	GTAGTCAGTGGTAATA-			M. leprae
1717	-GTGACGCAGGAAGGCAGCCGTACCA	GTAGTCAGTGGTAATA-			M. gastri
1660	-GTGACGCAGGAAGGCAGCCGTACCA	GTAGTCAGTGGTAATA-			M. kansasii
4111	-GTGACGCAGGAAGGTAGCCGTACCA	GTAGTCAGTGGTAATA-			M. smegmatis
	1730	1740	1750	1760	
1974	-CTGGGGCAAGCCGTAG--A	GAGCGATAGGCAAATCCGT	M. avium		
1974	-CTGGGGCAAGCCGTAG--A	GAGCGATAGGCAAATCCGT	M. paratuberc.		
2672	-CTGGGGCAAGCCGTAGGG	GAGCGATAGGCAAATCCGT	M. tuberculosis		
2063	-CGGGG	AAACCGTAGGGGAGAG	GATAGGCAAATCCGT	M. phlei	
1995	-CTGGAGCAAGCCGTAGGGAGAGCG	GATAGGCAAATCCGT	M. leprae		
1755	-CTGGGGCAAGCCGTAGGGAGAGCG	GATAGGCAAATCCGT	M. gastri		
1698	-CTGGGGCAAGCCGTAGGGAGAGCG	GATAGGCAAATCCGT	M. kansasii		
4149	-CGGGG	AAACCGTAGGGAGAGCG	GATAGGCAAATCCGT	M. smegmatis	

Figure 4H

24/31

	1810	1820	1830	1840	
2051	CG-AATTGGT GATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. avium
2051	CG-AATTGGT GATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. paratuberc.
2751	CG-AATTGGT GATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. tuberculosis
2141	CG-AATTGGT GATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. phlei
2074	CG-AATTGGT GATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. leprae
1834	CG-AATTGGT GATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. gastri
1777	CG-AATTGGT GATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. kansasii
4228	CG-AATTGGT GATCCTCTGCTGCCAAGAAAAGCCTCTA-				M. smegmatis
	1850	1860	1870	1880	
2089	GCGAGG ACATACAC GGCCCCGTACCCCAAACCAACACAGGT				M. avium
2089	GCGAGG CACATACAC GGCCCCGTACCCCAAACCAACACAGGT				M. paratuberc.
2789	GCGAGG CACACAC GGCCCCGTACCCCAAACCAACACAGGT				M. tuberculosis
2179	GCGAGG ACATACAC GGCCCCGTACCCCAAACCAACACAGGT				M. phlei
2112	GCGAGG ACATAC GGCCCCGTACCCCAAACCAACACAGGT				M. leprae
1872	GCGAGG CACACAC GGCCCCGTACCCCAAACCAACACAGGT				M. gastri
1815	GCGAGG CACACAC GGCCCCGTACCCCAAACCAACACAGGT				M. kansasii
4266	GCGAGG ACATACAC GGCCCCGTACCCCAAACCAACACAGGT				M. smegmatis
	1970	1980	1990	2000	
2208	AGGGGG CCCGGAATA TGGTGAACACCCTTGCGGTGGGAGC				M. avium
2208	AGGGGG CCCGGAATA TACCGTGAACACCCTTGCGGTGGGAGC				M. paratuberc.
2908	AGGGGG CCCGGAATA TGGTGAACACCCTTGCGGTGGGAGC				M. tuberculosis
2298	AGGGGG ACAC TACCGTGA GGG CTTGCGG GG AGC				M. phlei
2231	AGGGGG CCCGGAATA TGGTGAACACCCTTGCGGTGGGAGC				M. leprae
1910					M. gastri
1934	AGGGGG CCCGGAATA ACCGTGAACACCCTTGCGGTGGGAGC				M. kansasii
4385	AGGGGG ACAC AT GG CGTGA GG CC TT CGG CC AAGC				M. smegmatis
	2010	2020	2030	2040	
2248	GGGAT TGGG CGCAGAAACCAGT GG AGCGACT-GTTTA				M. avium
2248	GGGAT TGGG CGCAGAAACCAGT GG AGCGACT-GTTTA				M. paratuberc.
2948	GGGAT TGGG CGCAGAAACCAGT GG AGCGACT-GTTTA				M. tuberculosis
2338	GGGG TGGG CGCAGAAACCAGT GG AGCGACT-GTTTA				M. phlei
2271	GGGAT TGGG CGCAGAAACCAGT GG AGCGACT-GTTTA				M. leprae
1910					M. gastri
1974	GGGAT TGGG CGCAGAAACCAGT GG AGCGACT-GTTTA				M. kansasii
4425	GGGAT TGGG CGCAGAAACCAGT GG AGCGACT-GTTTA				M. smegmatis

Figure 4I

25/31

	2130	2140	2150	2160	
2367	CCGTTAACCGT	--AAGGGTGAAGCGGAGAATTAAAGCCC			M. avium
2367	CCGTTAACCGT	--AAGGGTGAAGCGGAGAATTAAAGCCC			M. paratuberc.
3067	CCGTTAACCGT	--AAGGGTGAAGCGGAGAATTAAAGCCC			M. tuberculosis
2457	CCGTTAACCC	TTTCGGGGGTGAAGCGGAGAATTAAAGCCC			M. phlei
2390	C T GTTAACCGT	--AAGGGTGAAGCGGAGAATTAAAGCCC			M. leprae
1910					M. gastri
2094	CCGTTAACCGT	--AAGGGTGAAGCGGAGAATTAAAGCCC			M. kansasii
4544	CCGTTAACCC	CTTGGGGGTGAAGCGGAGAATTAAAGCCC			M. smegmatis

- - -

	2250	2260	2270	2280	
2485	GTAACGACTT	CCAA CTGTCTCAACCATA	AGACTCGGGCAA		M. avium
2485	GTAACGACTT	CCCAC	ACTGTCTCAACCATA	AGACTCGGGCAA	M. paratuberc.
3185	GTAACGACTT	CCAA CTGTCTCAACCATA	AGACTCGGGCAA		M. tuberculosis
2577	GTAACGACTT	CCAA CTGTCTCAACCATA	AGACTCGGGCAA		M. phlei
2508	GTAACGACTT	CCAA CTGTCTCAACCATA	AGACTCGGGCAA		M. leprae
1910					M. gastri
2212	GTAACGACTT	CCAA CTGTCTCAACCATA	AGACTCGGGCAA		M. kansasii
4663	GTAACGACTT	CCAA CTGTCTAAC	A TAGACTCGGGCAA		M. smegmatis

- - -

	2370	2380	2390	2400	
2605	GTTCGGTACGGTT	TGTGTAGGATAGGTGGGAGACTTGAA			M. avium
2605	GTTCGGTACGGTT	TGTGTAGGATAGGTGGGAGACTTGAA			M. paratuberc.
3305	GTTCGGTACGGTT	TGTGTAGGATAGGTGGGAGACTTGAA			M. tuberculosis
2697	G T CG A TACGGTT	TGTGTAGGATAGGTGGGAGACTTGAA			M. phlei
2628	GTTCGGT	CGGTT TGTGTAGGATAGGTGGGAGACTTGAA			M. leprae
1910					M. gastri
2332	GTTCGGTACGGTT	TGTGTAGGATAGGTGGGAGACTTGAA			M. kansasii
4782	G T CG A TACGGTT	TGTGTAGGATAGGTGGGAGACTTGAA			M. smegmatis

Figure 4J

26/31

	2410	2420	2430	2440	
2645	G CACAGACGCCAGTTGGT G GAGTCGTTGAAATACC				M. avium
393	A TACAGACGCCAGTTGT T GGAGTCGTTGAAATACC				M. intracellulare
2645	G CACAGACGCCAGTTGT G GGAGTCGTTGAAATACC				M. paratuberc.
3345	A CCTGACGCCAGTTGG G GGAGTCGTTGAAATACC				M. tuberculosis
284	A CCTGACGCCAGTTGGGGGGAGTCGTTGAAATACC				M. bovis
2737	G CACGCCAGTTGGGGGGAGTCGTTGAAATACC				M. phlei
2668	A CCTGACGCCAGTTGGGGAGTCGTTGAAATACC				M. leprae
1910					M. gastri
2372	A CCTGACGCCAGTTGGGGAGTCGTTGAAATACC				M. kansasii
4822	G CACGCCAGTTGGGGAGTCGTTGAAATACC				M. smegmatis

	2450	2460	2470	2480	
2685	ACTCTGATCGTATTGGACACCTAACGTCGAACCT-TATC				M. avium
433	ACTCTGATCGTATTGGACACCTAACGTCGAACCT-TATC				M. intracellulare
2685	ACTCTGATCGTATTGGACACCTAACGTCGAACCT-TATC				M. paratuberc.
3385	ACTCTGATCGTATTGGCACTAACCTAACGTCGAACCT-TATC				M. tuberculosis
324	ACTCTGATCGTATTGGCACTAACCTAACGTCGAACCT-TATC				M. bovis
2777	ACTCTGATCGTATTGGCACTAACCTAACGTCGAACCT-TATC				M. phlei
2708	ACTCTGATCGTATTGGCACTAACCTAACGTCGAACCT-TATC				M. leprae
1910					M. gastri
2412	ACTCTGATCGTATTGGACACCTAACGTCGAACCT-TATC				M. kansasii
4862	ACTCTGATCGTATTGGCACTAACCTAACGTCGAACCT-TATC				M. smegmatis

	2690	2700	2710	2720	
2924	G GTGTC A CTCAACGGATAAAAGGTACCCGGGGATAACAG				M. avium
2924	GGTGTC A CTCAACGGATAAAAGGTACCCGGGGATAACAG				M. paratuberc.
3625	GGTGTC G CTCAACGGATAAAAGGTACCCGGGGATAACAG				M. tuberculosis
3017	GGTGTC G CTCAACGGATAAAAGGTACCCGGGGATAACAG				M. phlei
2948	GGTGTC G CTCAACGGATAAAAGGTACCCGGGGATAACAG				M. leprae
1910					M. gastri
2652	GGTGTC G CTCAACGGATAAAAGGTACCCGGGGATAACAG				M. kansasii
5102	GGTGTC G CTCAACGGATAAAAGGTACCCGGGGATAACAG				M. smegmatis

	2730	2740	2750	2760	
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTG				M. avium
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTG				M. paratuberc.
3665	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTG				M. tuberculosis
3057	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTG				M. phlei
2988	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTG				M. leprae
1910					M. gastri
2692	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTG				M. kansasii
5142	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTG				M. smegmatis

Figure 4K

27/31

	2770	2780	2790	2800	
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. avium
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. paratuberc.
3705	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. tuberculosis
3097	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. phlei
3028	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. leprae
1910					M. gastri
2732	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. kansasii
5182	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. smegmatis

	2810	2820	2830	2840	
3044	GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAGCGGCAC				M. avium
3044	GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAGCGGCAC				M. paratuberc.
3745	GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAGCGGCAC				M. tuberculosis
3137	GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAGCGGCAC				M. phlei
3068	GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAGCGGCAC				M. leprae
1910					M. gastri
2772	GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAGCGGCAC				M. kansasii
5222	GGTCCCAAGGGTTGGGCTGTTCGCCC-ATTAAGCGGCAC				M. smegmatis

	3050	3060	3070	3080	
3283	CAAGATCAGGTTT-CTCACCCATTAGGGATAAGGCC				M. avium
638	CAAGATCAGGTTT-CTCACCCATTAGGGATAAGGCC				M. intracellulare
3283	CAAGATCAGGTTT-CTCACCCATTAGGGATAAGGCC				M. paratuberc.
3984	CAAGATCAGGTTT-CTCACCCATTAGGGATAAGGCC				M. tuberculosis
570	CAAGATCAGGTTT-CTCACCCATTAGGGATAAGGCC				M. bovis
3376	CAAGATCAGGTTT-CTCACCCATTAGGGATAAGGCC				M. phlei
3307	CAAGATCAGGTTT-CTCACCCATTAGGGATAAGGCC				M. leprae
1910					M. gastri
3011	CAAGATCAGGTTT-CTCACCCATTAGGGATAAGGCC				M. kansasii
5462	CAAGATCAGGTTT-CTCACCCATTAGGGATAAGGCC				M. smegmatis

	3090	3100	3110	3120	
3322	CCCGC-AGACCACGGGATTGATAGGC	PAGACCTGGAAAGCT			M. avium
677	CCCGC-AGACCACGGGATTGATAGGC	PAGACCTGGAAAGCT			M. intracellulare
3322	CCCGC-AGATCACGGGATTGATAGGC	PAGACCTGGAAAGCT			M. paratuberc.
4023	CCCGC-AGAPCACGGGATTGATAGGC	PAGACCTGGAAAGCT			M. tuberculosis
609	CCCGC-AGAPCACGGGATTGATAGGC	PAGACCTGGAAAGCT			M. bovis
3415	CCCGC-AGACCACGGGATGATAGC	PCCAGACCTGGAAAGCT			M. phlei
3309					M. leprae
1910					M. gastri
3050	CCCGC-AGAPCACGGGATTGATAGC	PCCAGACCTGGAAAGCT			M. kansasii
5501	CCCGC-AGACCACGGGATTGATAGC	PCCAGACCTGGAAAGCT			M. smegmatis

Figure 4L

28/31

	130	140	150	160	
107	GAGTAACACGTGGC	C A	TGCCCC	TC	M. avium
59	GAGTAACACGTGGG	CA	ATCTGC	CCCTGC	M. intracellulare
107	GAGTAACACGTGGG	CA	ATCTGC	CCCTGC	M. paratuberc.
70	GAGTAACACGTGGG	CA	ATCTGC	CCCTGC	M. scrofulaceum
70	GAGTAACACGTGGG	CA	ATCTGC	CCCTGC	M. tuberculosis
209	GAGTAACACGTGGG	CA	ATCTGC	CCCTGC	M. bovis
120	GAGTAACACGTGGG	CA	ATCTGC	CCCTGC	M. leprae
69	GAGTAACACGTGGG	CA	ATCTGC	CCCTGC	M. kansasii
70	GAGTAACACGTGGG	CA	ATCTGC	CCCTGC	M. gastri
104	GAGTAACACGTGGG	CA	ATCTGC	CCCTGC	M. gordonae
64	GAGTAACACGTGGG	CA	ATCTGC	CCCTGC	M. marinum

	450	460	470	480	
424	AAACCTCTTCACC	ATCGACGA	AGGTCCGGG	TTTT CTCGG	M. avium
376	AAACCTCTTCACC	ATCGACGA	AGGTCCGG	TTTTCTCGG	M. intracellulare
424	AAACCTCTTCACC	ATCGACGA	AGGTCCGG	TTTTCTCGG	M. paratuberc.
387	AAACCTCTTCACC	ATCGACGA	AGGTCCGG	CTCA TTTGTCGG	M. scrofulaceum
389	AAACCTCTTCACC	ATCGACGA	AGGTCCGG	TTCTCGG	M. tuberculosis
528	AAACCTCTTCACC	ATCGACGA	AGGTCCGG	TTCTCGG	M. bovis
439	AAACCTCTTCACC	ATCGACGA	AGGTCCGG	CTGG TTCTCGG	M. leprae
386	AAACCTCTTCACC	ATCGACGA	AGGTCCGG	TTCTCGG	M. kansasii
387	AAACCTCTTCACC	ATCGACGA	AGGTCCGG	TTCTCGG	M. gastri
420	AAACCTCTTCACC	ATCGACGA	AGGTCCGG	TTCTCGG	M. gordonae
381	AAACCTCTTCACC	ATCGACGA	AGGTCCGG	TTCTCGG	M. marinum
	490	500	510	520	
429	ATTGACGGTAGGTG	GAGAAGAAG	ACCGGCC	ACTACGTG	M. tuberculosis
568	ATTGACGGTAGGTG	GAGAAGAAG	ACCGGCC	ACTACGTG	M. bovis
464	ATTGACGGTAGGTG	GAGAAGAAG	ACCGGCC	ACTACGTG	M. avium
416	ATTGACGGTAGGTG	GAGAAGAAG	ACCGGCC	ACTACGTG	M. intracellulare
464	ATTGACGGTAGGTG	GAGAAGAAG	AC -----	ACTACGTG	M. paratuberc.
424	ATTGACGGTAGGTG	GAGAAGAAG	ACCGGCC	ACTACGTG	M. scrofulaceum
479	ATTGACGGTAGGTG	GAGAAGAAG	ACCGGCC	ACTACGTG	M. leprae
426	ATTGACGGTAGGTG	GAGAAGAAG	ACCGGCC	ACTACGTG	M. kansasii
427	ATTGACGGTAGGTG	GAGAAGAAG	ACCGGCC	ACTACGTG	M. gastri
460	GTGACGGTAGGTG	GAGAAGAAG	ACCGGCC	ACTACGTG	M. gordonae
421	ATTGACGGTAGGTG	GAGAAGAAG	ACCGGCC	ACTACGTG	M. marinum

Figure 5A

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	1130	1140	1150	1160	
1104	TCTCATGTTGCCAG	GGGTAAATGC	GGGGACTCGTGAGAG		M. avium
1056	TCTCATGTTGCCAGC	GGGGTAATGCCGGGACTCGTGAGAG			M. intracellulare
1098	TCTCATGTTGCCAGC	GGGGTAATGCCGGGACTCGTGAGAG			M. paratuberc.
1064	TCTCATGTTGCCAGC	GGGGTAATGCCGGGACTCGTGAGAG			M. scrofulaceum
1069	TCTCATGTTGCCAGC	GGGGTAATGCCGGGACTCGTGAGAG			M. tuberculosis
1208	TCTCATGTTGCCAGC	GGGGTAATGCCGGGACTCGTGAGAG			M. bovis
1119	TCTCATGTTGCCAGC	GGGGTAATGCCGGGACTCGTGAGAG			M. leprae
1066	TCTCATGTTGCCAGC	GGGGTAATGCCGGGACTCGTGAGAG			M. kansasii
1067	TCTCATGTTGCCAGC	GGGGTAATGCCGGGACTCGTGAGAG			M. gastri
1100	TCTCATGTTGCCAGC	GGGGTAATGCCGGGACTCGTGAGAG			M. gordonae
1061	TCTCATGTTGCCAGC	GGGGTAATGCCGGGACTCGTGAGAG			M. marinum
- - -					
	1290	1300	1310	1320	
1264	CGAATCCTTTA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. avium
1216	CGAATCCTTTA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. intracellulare
1258	CGAATCCTTTA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. paratuberc.
1224	CGAATCCTTTA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. scrofulaceum
1229	CGAATCCTTTA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. tuberculosis
1368	CGAATCCTTAA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. bovis
1279	CGAATCCTTAA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. leprae
1226	CGAATCCTTAA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. kansasii
1227	CGAATCCTTAA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. gastri
1260	CGAATCCTTAA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. gordonae
1221	CGAATCCTTAA	AAAGCCGGACTCAGTCGGAT	GGGGTCT		M. marinum
	1330	1340	1350	1360	
1304	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. avium
1256	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. intracellulare
1298	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. paratuberc.
1264	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. scrofulaceum
1268	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. tuberculosis
1407	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. bovis
1319	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. leprae
1266	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. kansasii
1267	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. gastri
1300	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. gordonae
1260	GCAACTCGACCC	ATGAAGTCGGAGTCGCTAGTAATCGCA			M. marinum

Figure 5B

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Mavirus 23S:
TTACGGCGGCAGGACGA²⁵⁸⁹AAGACCCGGGACCTTCACTA
2550 2568 2569 2589

Figure 6

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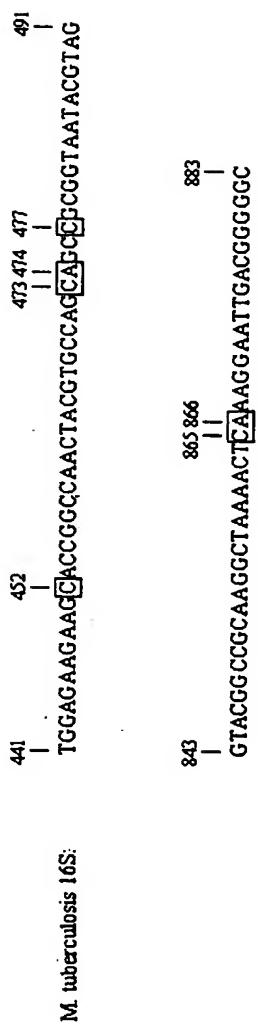


Figure 7